

Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID:1)

1 GATCACAGTC TTTGTATTTT TCTACTTCTG CCTTTAGCTG TTCCCTTTGG TCTCGAAGTG
61 AAGAAAGCTC TTTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTTAGCTT
121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAC TGAGATTCCA
181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTTACT TGGAAAAGCC CAATAATAAT
241 TAGAAGTTCC GATC

Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO:2) and amino acid sequence (SEQ ID. NO:3) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

1 ccaaaatcaaacgcgtccgggctgtcccgcccctctccccaagcgcgggcccgccagc
1 M S K K K G L S A E E K R
61 ggaagccccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAGAGCTTTCTTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I R Q A N K V A K E A A N R W T D N I
541 GAAATACGCCAAGCAAATAAAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATA
174 F A I K S W A K R K F G F E E N K I D R
601 TTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGA
194 T F G I P E D F D Y I D *
661 ACTTTTGAATTCCAGAAGACTTTGACTACATAGACTAAAtattccatggtggtgaagg
721 atgtacaagcttgtgaatatgtaaatttttaaactattatctaactaagtgtactgaattg
781 tcgtttgcctgttaactgtgtttatcatttttattaatgttaaataaagtgtaaaatgcaaa
841 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa



Figure 2B. The cDNA (SEQ ID. NO:4) and amino acid sequence (SEQ ID. NO:5) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

```
1 ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcggggcccgccagc
1 M S K K K G L S A E E K R
61 ggaagcccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q D
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGGAC
94 P G C C F H E I I K V S Y Y R K F W L G
361 CCTGGCTGCTGCTTCCATGAAATAATTAAAGTCTCCTATTATAGAAAATTCTGGCTGGGC
114 A V A H A C N P S T L G G *
421 GCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAggcgggcagatcacgagg
481 tgactttccccccacccccacatgaagtgaagatggagttgtctgaggggaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggccgatgtgaaacggaagagc
601 gaaccaggctagcaaaagagctttcttcacttcgagaccaaagggaacagctaaaggcag
661 aagtagaaaaatacaaaagactgtgatccgcaagttgtggaagaaatacgccaagcaaata
721 aagtagccaaagaagctgctaacagatggactgataacatattcgcaataaaatcttggg
781 ccaaaagaaaatttgggtttgaagaaaataaaattgatagaacttttggaattccagaag
841 actttgactacatagactaaaatattccatgggtggaaggatgtacaagcttgtgaata
901 tgtaaatttttaaactattatctaactaagtgtactgaattgtcgtttgctgttaactgtg
961 tttatcattttattaatgttaaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa
```

Figure 2C. The cDNA (SEQ ID. NO:6) and amino acid sequence (SEQ ID.NO:7) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

```

1  ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcggggcccgccagc
61  ggaagcccctgcgcccgcgccatgtcaaagaaaaaaggactgagtgcagaagaaaagaga
121 actcgcgatgatggaaatatcttctgaaacaaaagatgtatttcaattaaaagacttggag
181 aagattgctcccaaagagaaaggcattactgctatgtcagtaaaagaagtccttcaaagc
241 ttagttgatgatggtatggttgactgtgagaggatcggaacttctaattattattgggct
301 tttccaagtaaagctcttcatgcaaggaaacataagttggagggttctggaatctcaggac
361 cctggctgctgcttccatgaaataattaaagtctcctattatagaaaattctggctgggc
421 gcagtggctcacgcctgtaatcccagcactttgggaggctgaggcgggcagatcacgagg
1      M K C K M E L S E G S Q K H
481 tgactttccccccaccccccacATGAAGTGCAAGATGGAGTTGTCTGAGGGAAGTCAAAGC
15  A S L Q K S I E K A K I G R C E T E E R
541 ATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC
35  T R L A K E L S S L R D Q R E Q L K A E
601 GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAG
55  V E K Y K D C D P Q V V E E I R Q A N K
661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATA
75  V A K E A A N R W T D N I F A I K S W A
721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGG
95  K R K F G F E E N K I D R T F G I P E D
781 CCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGAATTCCAGAAG
115  F D Y I D *
841 ACTTTGACTACATAGACTAAaataattccatggtggtgaaggatgtacaagcttgtgaata
901 tgtaaattttaaaactattatctaactaagtgtactgaattgtcgtttgctgtgaactgtg
961 tttatcatttttattaatgttaaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa

```

Figure 2D. The cDNA (SEQ ID. NO:8) and amino acid sequence (SEQ ID. NO:9) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

```
1 ccaaaatcaaacgcgtccgggacctgtcccgccctctccccaagcgcgggccccggccagc
1                               M S K K K G L S A E E K R
61 ggaagccccctgcgcccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T A K Q I K *
421 CGATGTGAAACGGCCAAGCAAATAAAGTAGccaaagaagctgctaacagatggactgata
481 acatattcgcaataaaaatcttgggccaaaagaaaatttgggtttgaagaaaataaaattg
541 atagaacttttgggaattccagaagactttgactacatagactaaaatattccatggtggt
601 gaaggatgtacaagcttgtgaatatgtaaattttaaactattatctaactaagtgtactg
661 aattgtcgtttgcctgttaactgtgtttatcattttattaatgttaaataaagtgtaaaat
721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

Figure 2E. The cDNA (SEQ ID. NO:10) and amino acid sequence (SEQ ID. NO:11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

```

1  ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcgggccccggccagc
1                               M S K K K G L S A E E K R
61  ggaagccccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAAGAAAGAGA
14  T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34  K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCTTCAAAGC
54  L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
74  F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94  S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I H N I F A I K S W A K R K F G F E E
541 GAAATACATAACATATTTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAA
174 N K I D R T F G I P E D F D Y I D *
601 AATAAAATTGATAGAACTTTTGGGAATCCAGAAGACTTTGACTACATAGACTAAaatatt
661 ccatggtggtgaaggatgtacaagcttgtgaatatgtaaattttaactattatctaact
721 aagtgtactgaattgtcgtttgccctgtaactgtgtttatcattttattaatgttaaataa
781 agtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

```

Figure 2F. The cDNA (SEQ ID. NO:12) and amino acid sequence (SEQ ID. NO:13) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

```

1  gttttctgtattgtaatatgtagagcacattccagaactgctcagtttctgagttacctaa
61  tggatcttccactgtgtgccaattagtcgatttctgtgaaaacgccccggtttctgcaaaa
121 gggcaggagtcgctgctcttgtgccgggtgctgctggttggtgtagggcgctgttgctttt
181 ttaaggacgctctgcactgaattaggcttctctcgctgggtcatgatcagttaagtcctgtc
1      M M E I F S E
241 aaagaaaaaaggactgagtgacagaagaaaagagaactcgcatATGATGGAAATATTTTCTGA
8  T K D V F Q L K D L E K I A P K E K G I
301 AACAAAAGATGTATTTCAATTAAGACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT
28  T A M S V K E V L Q S L V D D G M V D C
361 TACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGCTTAGTTGATGATGGTATGGTTGACTG
48  E R I G T S N Y Y W A F P S K A L H A R
421 TGAGAGGATCGGAACCTCTAATTATTATTGGGCTTTTCCAAGTAAAGCTCTTCATGCAAG
68  K H K L E V L E S Q L S E G S Q K H A S
481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAAGCATGCAAG
88  L Q K S I E K A K I G R C E T E E R T R
541 CCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCAG
108 L A K E L S S L R D Q R E Q L K A E V E
601 GCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAGAAAGTAGA
128 K Y K D C D P Q V V E E I R Q A N K V A
661 AAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATAAAGTAGC
148 K E A A N R W T D N I F A I K S W A K R
721 CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGGCCAAAAG
168 K F G F E E N K I D R T F G I P E D F D
781 AAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGAATTCCAGAAGACTTTGA
188 Y I D *
841 CTACATAGACTAAaatattccatgggtggtgaaggatgtacaagcttgtgaatatgtaaat
901 tttaaactattatctaactaagtgtactgaattgtcgtttgctgtgaactgtgtttatca
961 ttttattaatgttaataaagtgtaaaatgcagatgttcttcaccccttttggtagaaca
1021 aaagcaggatgataaccatataccccccagtgtcatcaaagtaggacactaaaaatccat
1081 ccatctcagtcaaagtcgagcgccgcgaatttagtagtagtagcgggccgctctagagga
1141 tccaagcttacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattc
1201 aagtt

```

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO:14). The 121P1F1 protein has 205 amino acids.

```
1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA
181 KRKFGFEENK IDRTFGIPED FDYID
```

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO:15). The 121P1F1 splice variant 1A protein has 126 amino acids.

```
1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVAHACN
121 PSTLGG
```

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO:16). The 121P1F1 splice variant 1B protein has 119 amino acids.

```
1 MKCKMELSEG SQKHASLQKS IEKAKIGRCE TEERTRLAKE LSSLRDQREQ LKAEVEKYKD
61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID
```

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO:17). The 121P1F1 splice variant 2 protein has 122 amino acids.

```
1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ
121 IK
```

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO:18). The 121P1F1 splice variant 3 protein has 190 amino acids.

```
1  MSKKKGLSAE  EKRTRMMEIF  SETKDVFLQK  DLEKIAPKEK  GITAMSVKEV  LQSLVDDGMV
61  DCERIGTSNY  YWAFPSKALH  ARKHKLEVLE  SQLSEGSQKH  ASLQKSIEKA  KIGRCETEER
121  TRLAKELSSL  RDQREQLKAE  VEKYKDCDPQ  VVEEIHNIFA  IKSWAKRKFG  FEENKIDRTF
181  GIPEDFDYID
```

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO:19). The 121P1F1 splice variant 4 protein has 190 amino acids.

```
1  MMEIFSETKD  VFQLKDLEKI  APKEKGITAM  SVKEVLQSLV  DDGMVDCERI  GTSNYYWAFP
61  SKALHARKHK  LEVLESQISE  GSQKHASLQK  SIEKAKIGRC  ETEERTRLAK  ELSSLRDQRE
121  QLKAEVEKYK  DCDPQVVEEI  RQANKVAKEA  ANRWTDNIFA  IKSWAKRKFG  FEENKIDRTF
181  GIPEDFDYID
```


Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SEQ ID NOS: 3, 5, 7, 9 and 11)

```

121P1F01      -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLEKIAPKEKGITAMSVKE
sv1A          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLEKIAPKEKGITAMSVKE
sv1B          -----MKCKMELSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
sv-2          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLEKIAPKEKGITAMSVKE
sv-3          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLEKIAPKEKGITAMSVKE

121P1F01      VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQK-HASLQKS-I
sv1A          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQDP-GCCF-HEI IKVSYY
sv1B          QLKAEVEK-YKDCDPQVVEEIRQANKVAKEAANRWTDNIFAISWAKRKFGFEENKID--
sv-2          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQK-HASLQKS-I
sv-3          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQK-HASLQKS-I

121P1F01      EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAAN
sv1A          RKFWLGAVAHACNPSTLGG-----
sv1B          RTFGIPEDFDYID-----
sv-2          EKAKIGRCETAKQIK-----
sv-3          EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIHNI FAIKSWAKR

121P1F01      RWTDNIFAISWAKRKFGFEENKIDRTFGIPEDFDYID
sv1A          -----
sv1B          -----
sv-2          -----
sv-3          KFGFEENKIDRTFGIPEDFDYID-----

```

Figure 4B

B) Clustal alignment of 121P1F1 and variants 1A and 4 (SEQ ID NOS 3, 13 and 5)

```

1 121P1F01      1      15 16      30 31      45 46      60 61      75 76      90
2 sv-4          -----MMEIFSETKDVFLQK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCERIGTSNYYWAF SKALHARKHKLEVLE
3 sv-1A         MSKKKGLSAEEKRTR MMEIFSETKDVFLQK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCERIGTSNYYWAF SKALHARKHKLEVLE
-
1 121P1F01      91      105 106      120 121      135 136      150 151      165 166      180
2 sv-4          SQLSEGSQKHASLQK SIEKAKIGRCETEER TRLAKELSSLRDQRE QLKAEVEKYKDCDPQ VVEEIRQANKVAKEA ANRWTDNIFAISWA
3 sv-1A         SQDPGCCFHEI IKVS YRKFWLG----- -----AVAHACNPS TLGG-----
-
1 121P1F01      181      195 196      210 211
2 sv-4          KRKFGFEENKIDRTF GIPEDFDYID 205
3 sv-1A         ----- 190

```

Figure 4C**C) Alignment of 121P1F1 and variant 1 (SEQ ID NO:20) with human GAJ (SEQ ID NO:21)**

Identities = 205/205 (100%), Positives = 205/205 (100%)

```
121P1: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGRCETEER 120
          DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGRCETEER
Sbjct: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGRCETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA 180
          TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA
Sbjct: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEENKIDRTFGIPEDFDYID
Sbjct: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
```

Figure 4D

D) Alignment of 121P1F1 and variant 1 (SEQ ID NO:22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO:23)

Identities = 183/205 (89%), Positives = 193/205 (93%)

```

121P1: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKK+GLS EEKTRMMEIF ETKDVFLKDLEK+APKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1   MSKKRGLSGEEKRTRMMEIFFETKDVFLKDLEKLAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGRCETEER 120
          DCERIGTSNYYWAFPSKALHARK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER
Sbjct: 61   DCERIGTSNYYWAFPSKALHARKRKLEALNSQSEGSQKHADLQKSIEKARVGRQETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA 180
          LAKEL S RDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANRWDNIFAISWA
Sbjct: 121  AMLAKELFSFRDQRQQLKAEVEKYRECDPQVVEEIREANKVAKEAANRWDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEE+KID+ FGIPEDFDYID
Sbjct: 181  KRKFGFEESKIDKNFGIPEDFDYID 205

```

Figure 4E

E) Alignment of 121P1F1 and variant 1 (SEQ ID NO:24)

with>gi|1175412|sp|Q09739|YA53_SCHPO HYPOTHETICAL 24.2 KD
PROTEIN C13A11.03 IN CHROMOSOME I (SEQ ID NO:25)

gi|7490680|pir||T37610 hypothetical coiled-coil protein -
fission yeast

(Schizosaccharomyces pombe)

gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil
protein [Schizosaccharomyces pombe]

Length = 210

Score = 121 bits (305), Expect = 5e-27

Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps =
6/202 (2%)

Query: 5

KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64

KGLS EKR R+ IF ++KD FQLK++EK+ K K I

+VK+VLQSLVDD +V E+

Sbjct: 4 KGLSLAEKRRRLEAIFHDSKDDFFQLKEVEKLGSK-

KQIVLQTVKDVQLQSLVDDNIVKTEK 62

Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESQ LSEGSQKHASLQKSIEKAKIGR--
--CETEER 120

IGTSNYYW+FPS A +R+ L L++QL + QK +L ++I K R

E +

Sbjct: 63

IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTEENDAN

122

Query: 121

TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA
180

+ L + + + LK ++ C+P+ E + K EAAN WTD

I + ++

Sbjct: 123

QYTLELLHAKESSELKLLKTQLSNLNHCNPETFELKNENTKKYMEAAANLWTDQIHTLIAFC

182

Query: 181 KRKFGFEENKIDRTFGIPEDFD 202

R G + N+I IPED D

Sbjct: 183 -RDMGADTNQIREYCSIPEDLD 203

Figure 5A
121P1F1 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

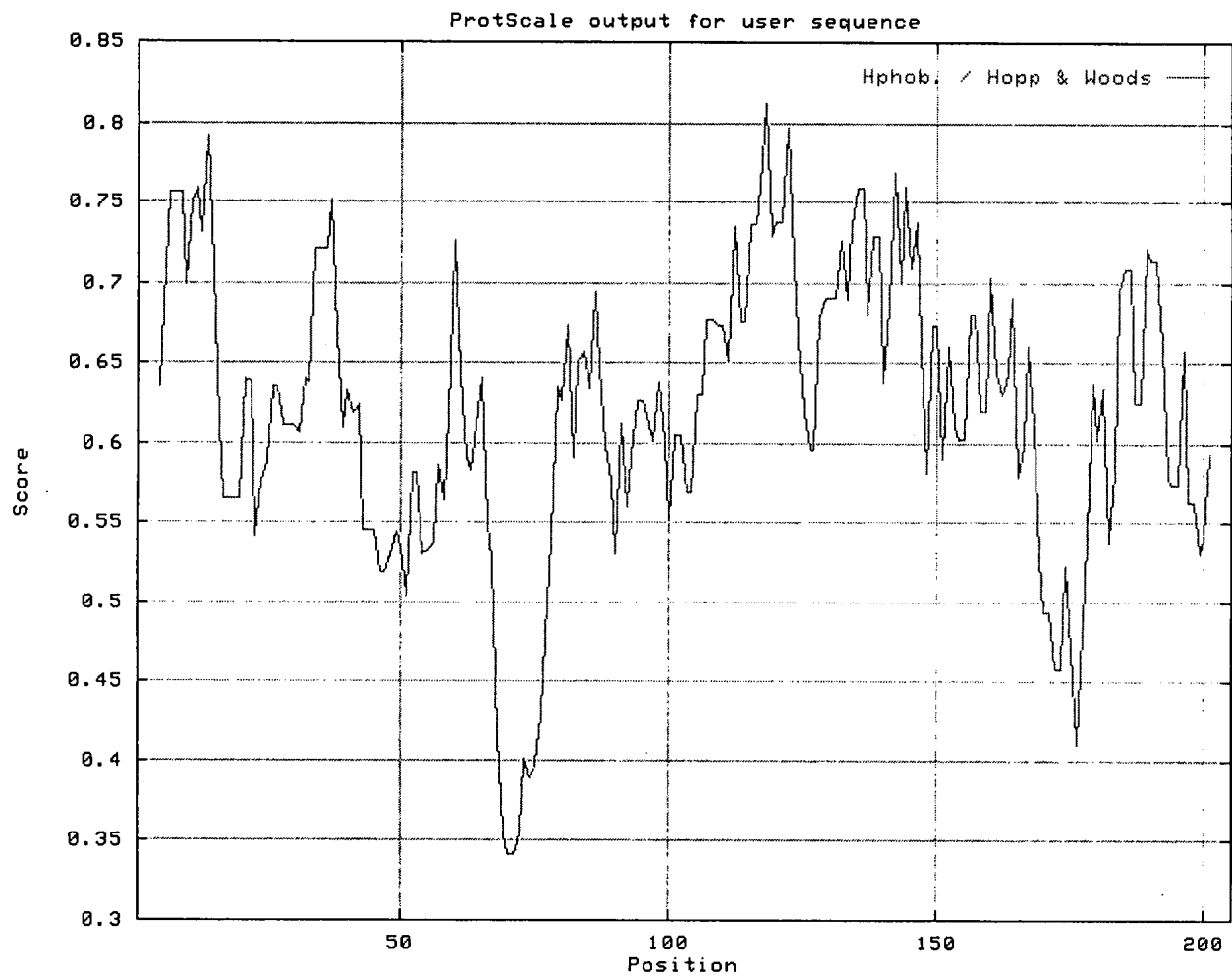


Figure 5B
121P1F1 variant 1a Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

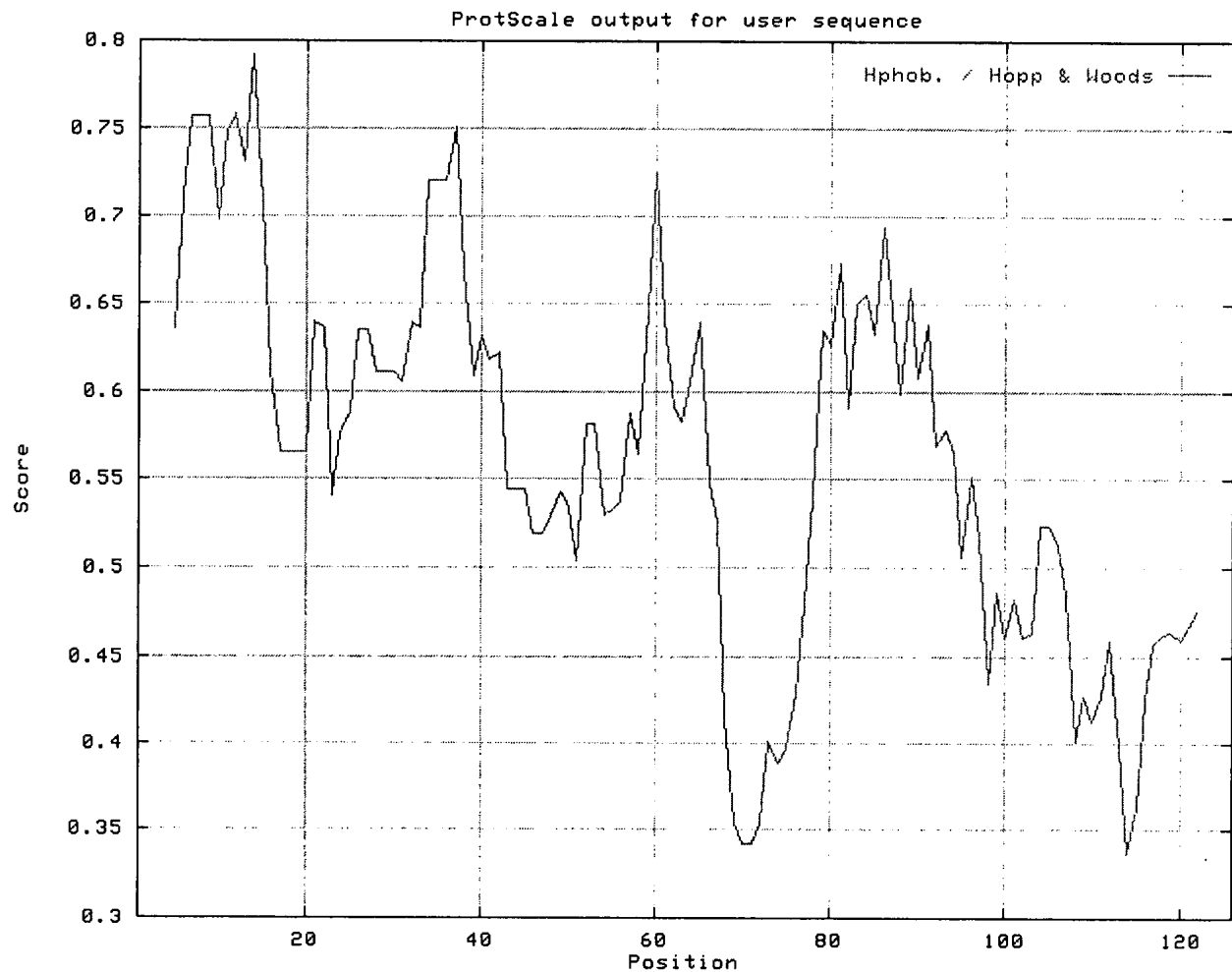


Figure 6A
121P1F1 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

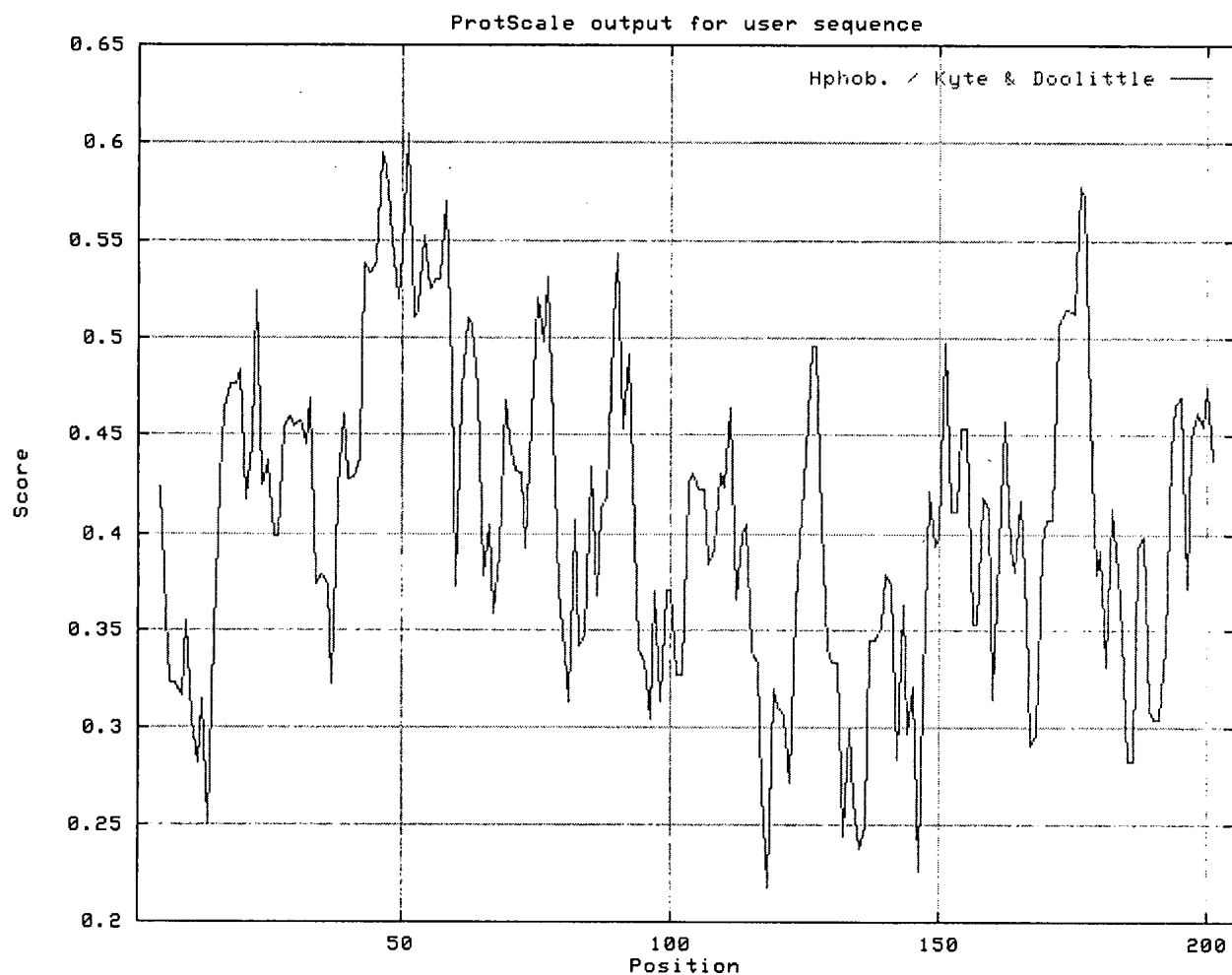


Figure 6B

121P1F1 variant 1a Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

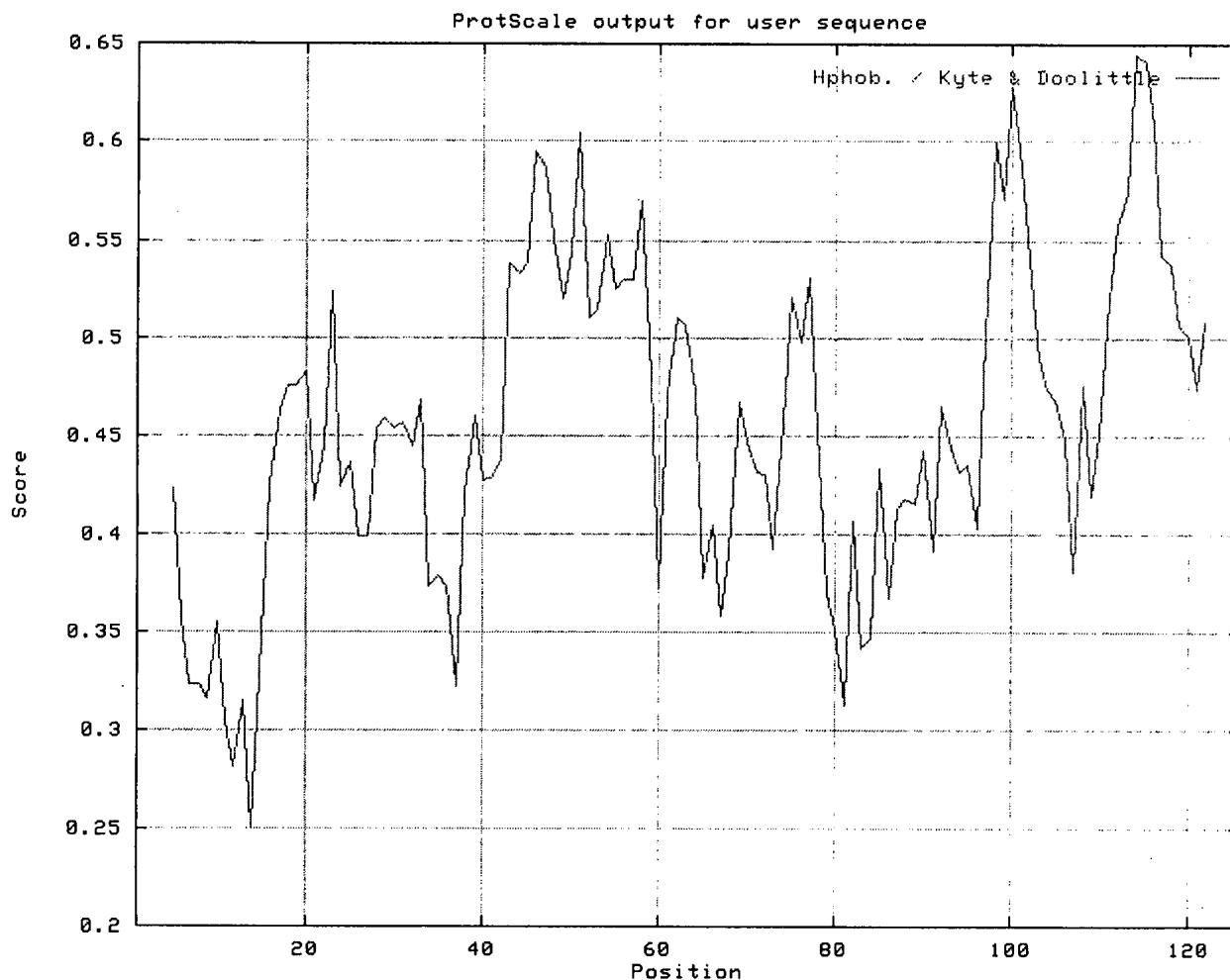


Figure 7A

121P1F1 % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

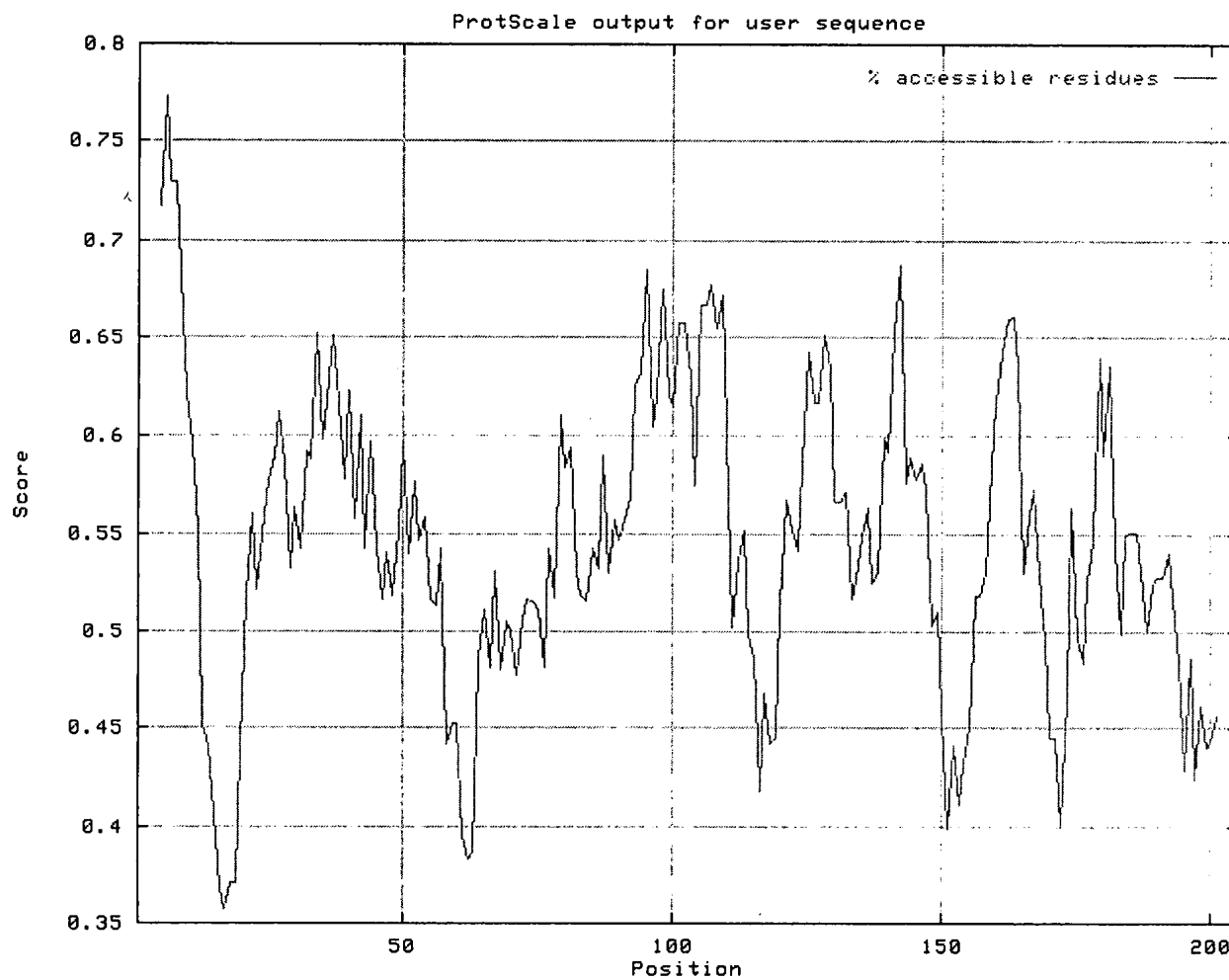


Figure 7B
121P1F1 variant 1a % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

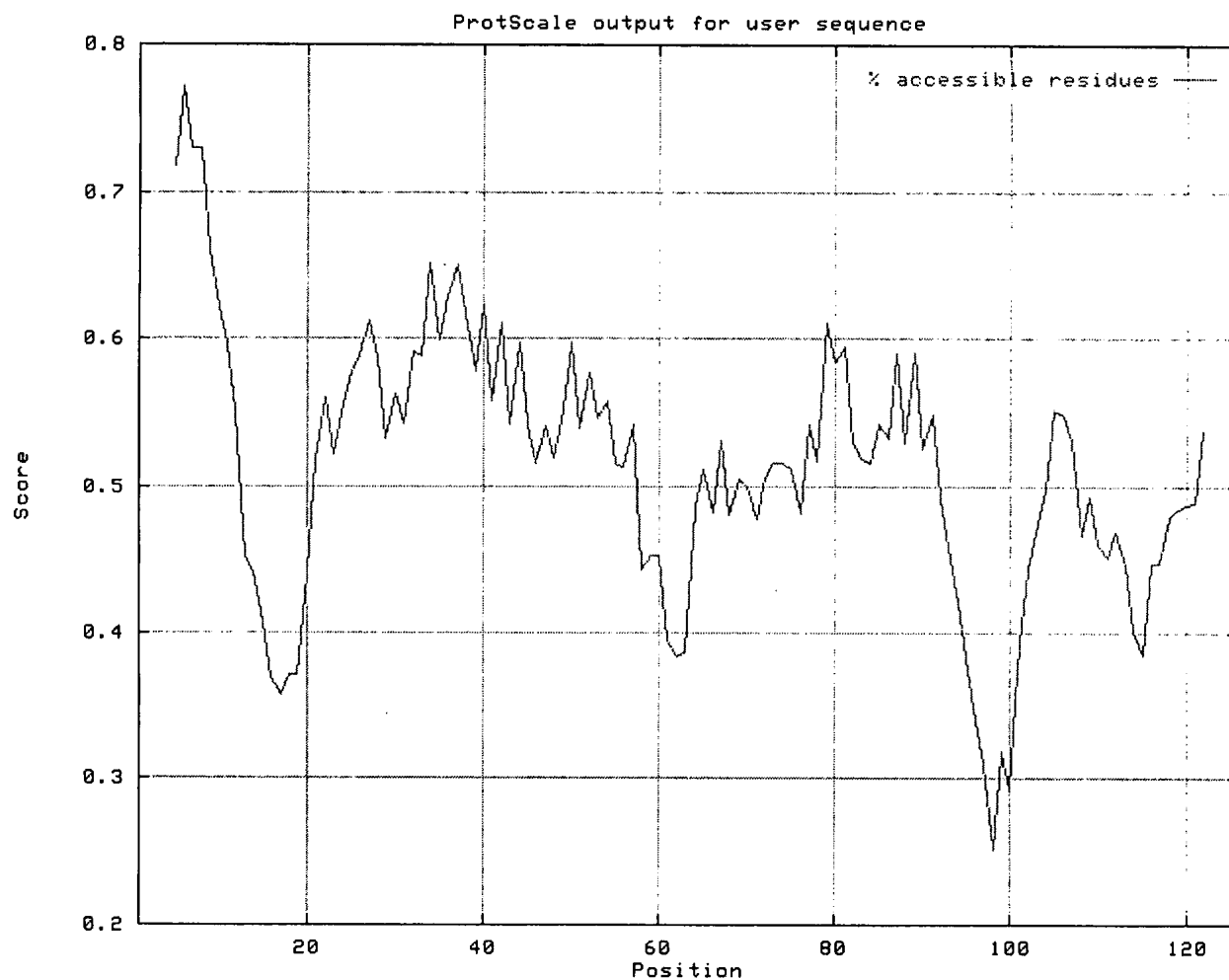


Figure 8A
121P1F1 Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

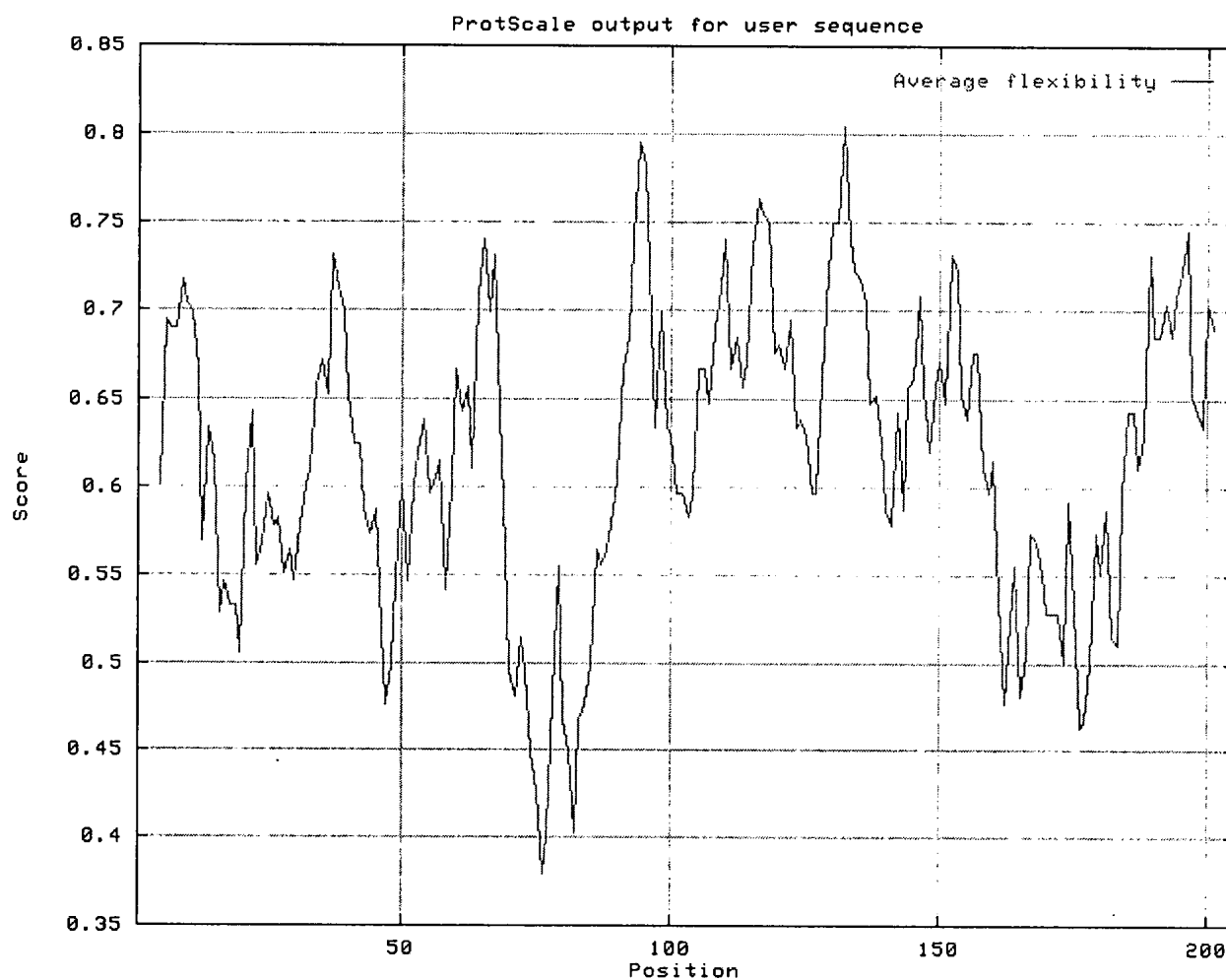


Figure 8B

121P1F1 variant 1a Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

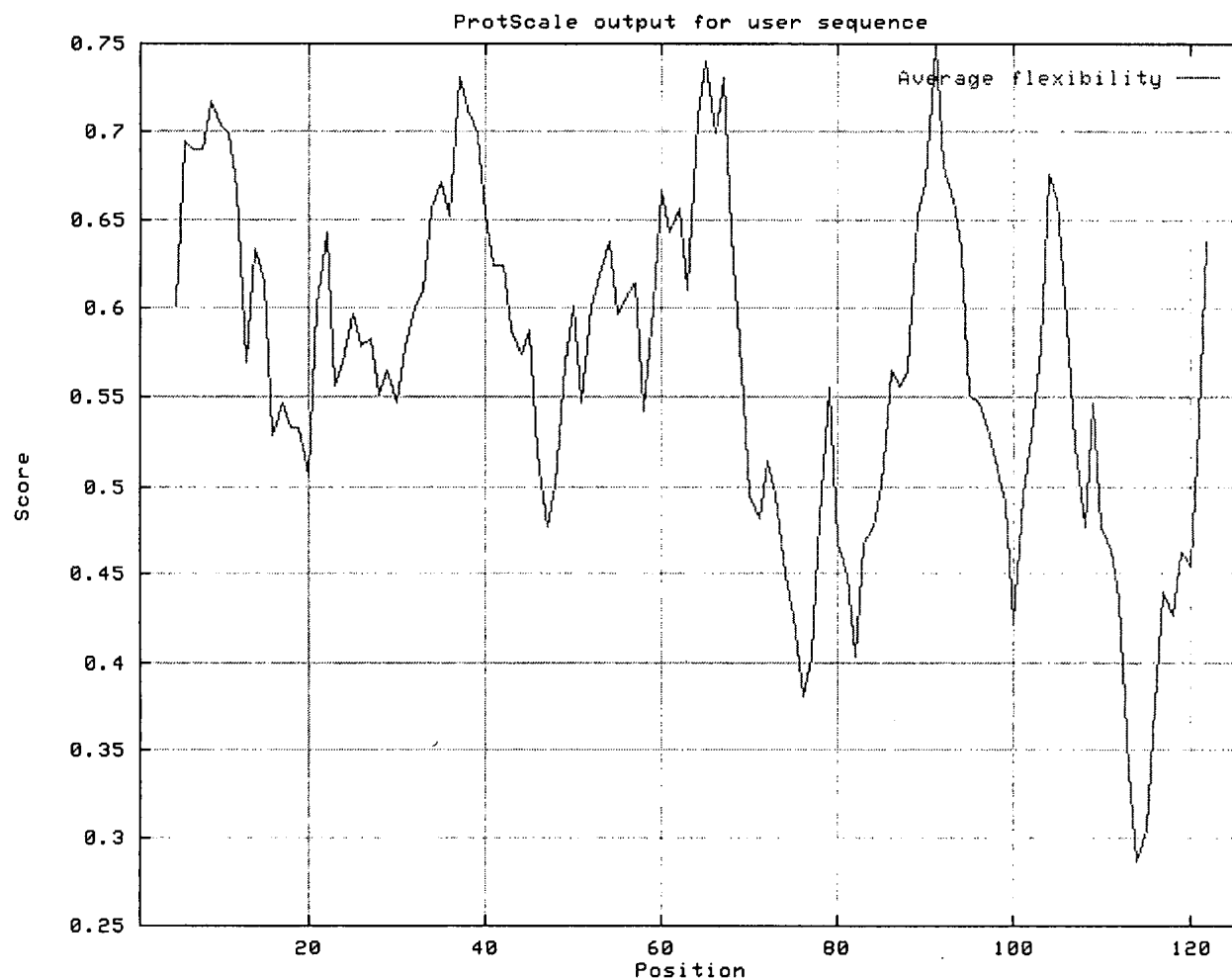


Figure 9A

121P1F1 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

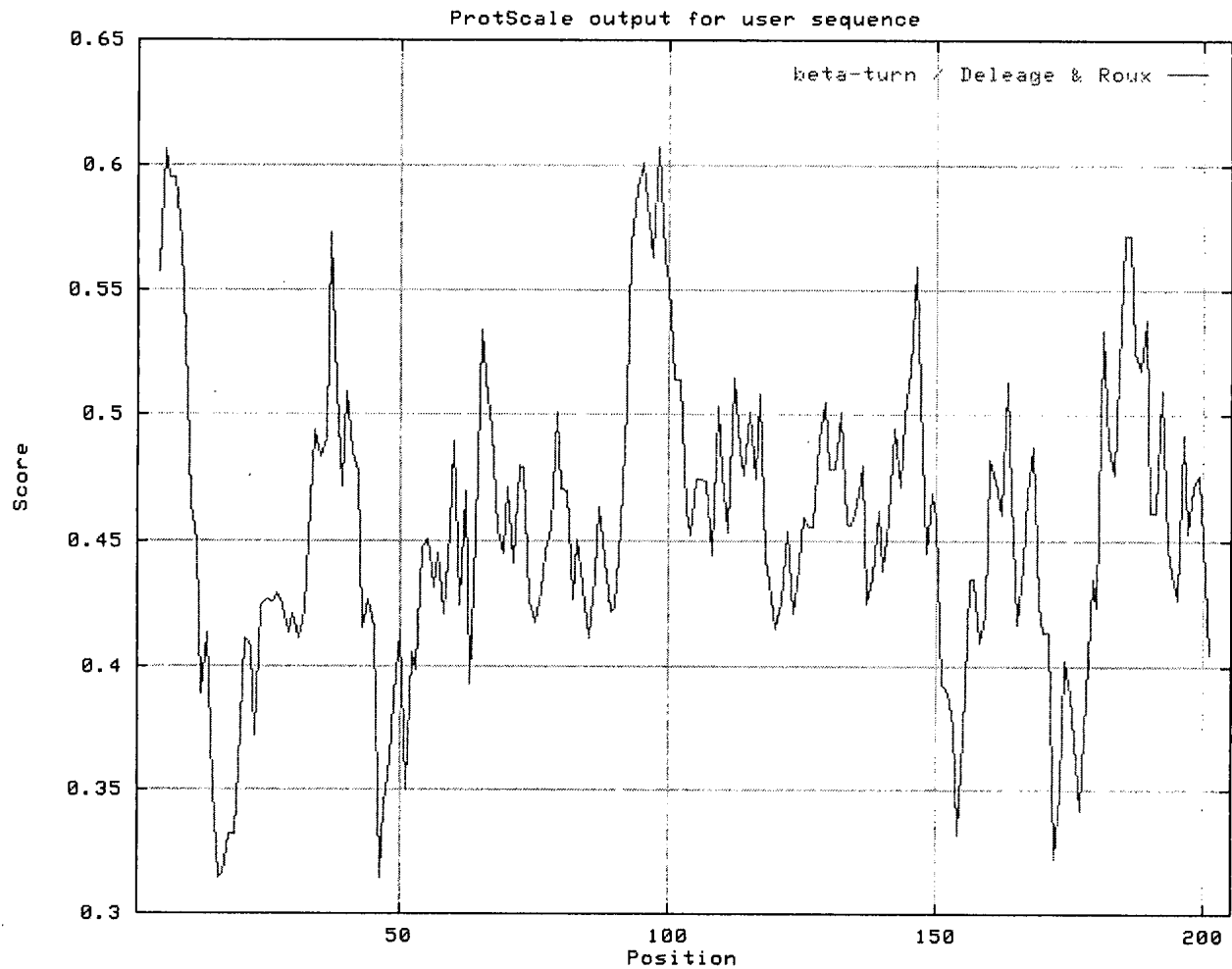


Figure 9B

121P1F1 variant 1a Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

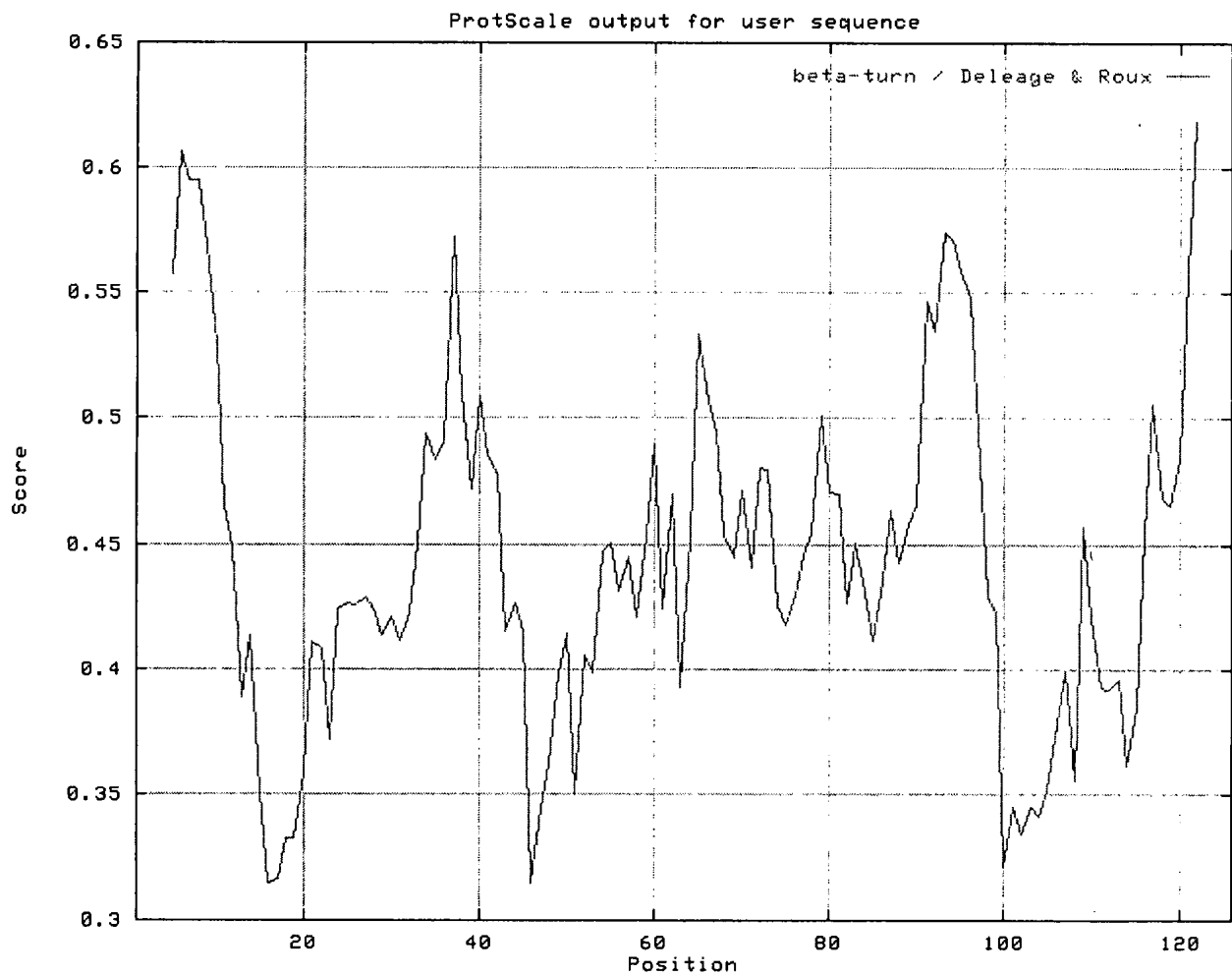
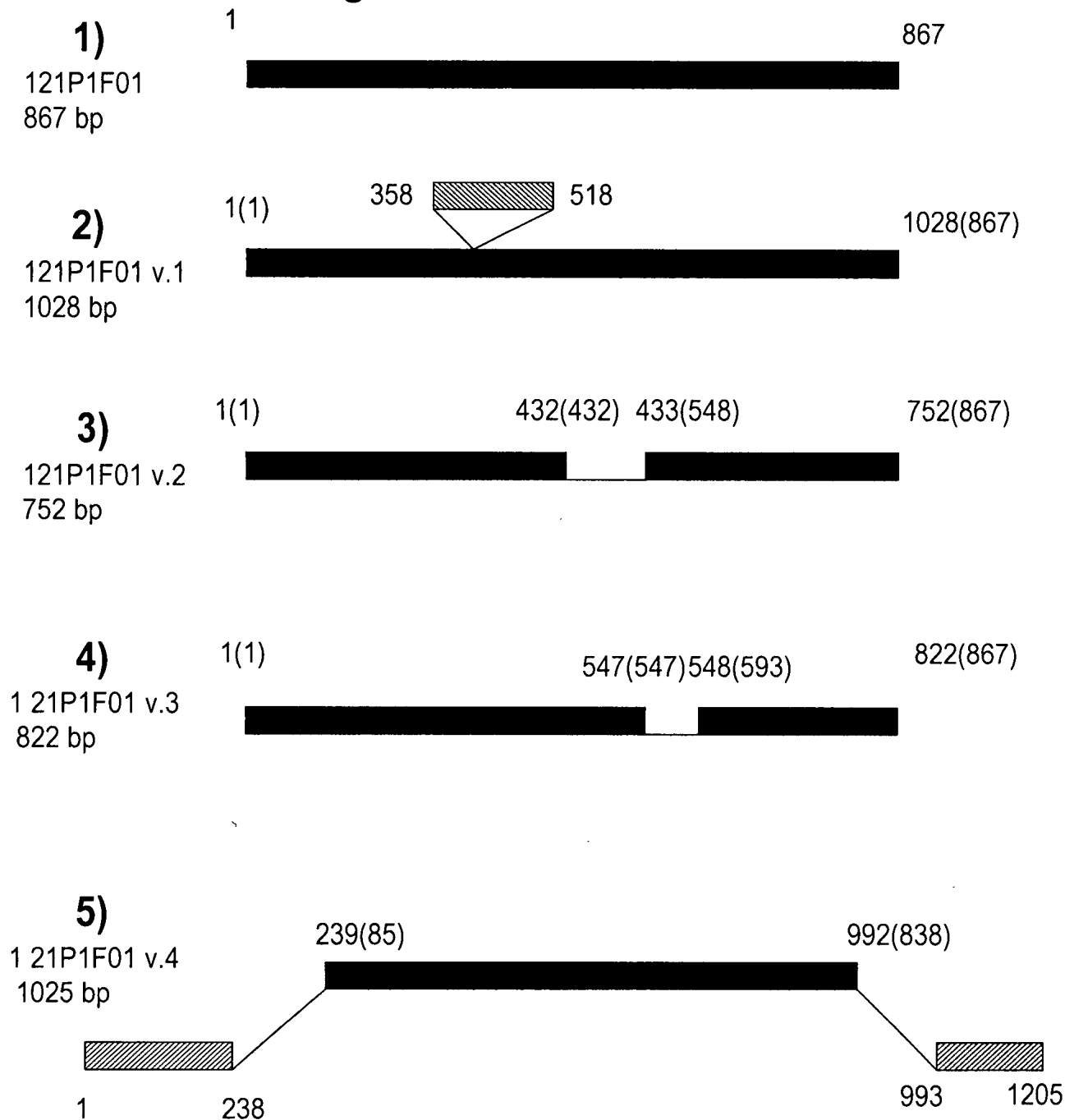
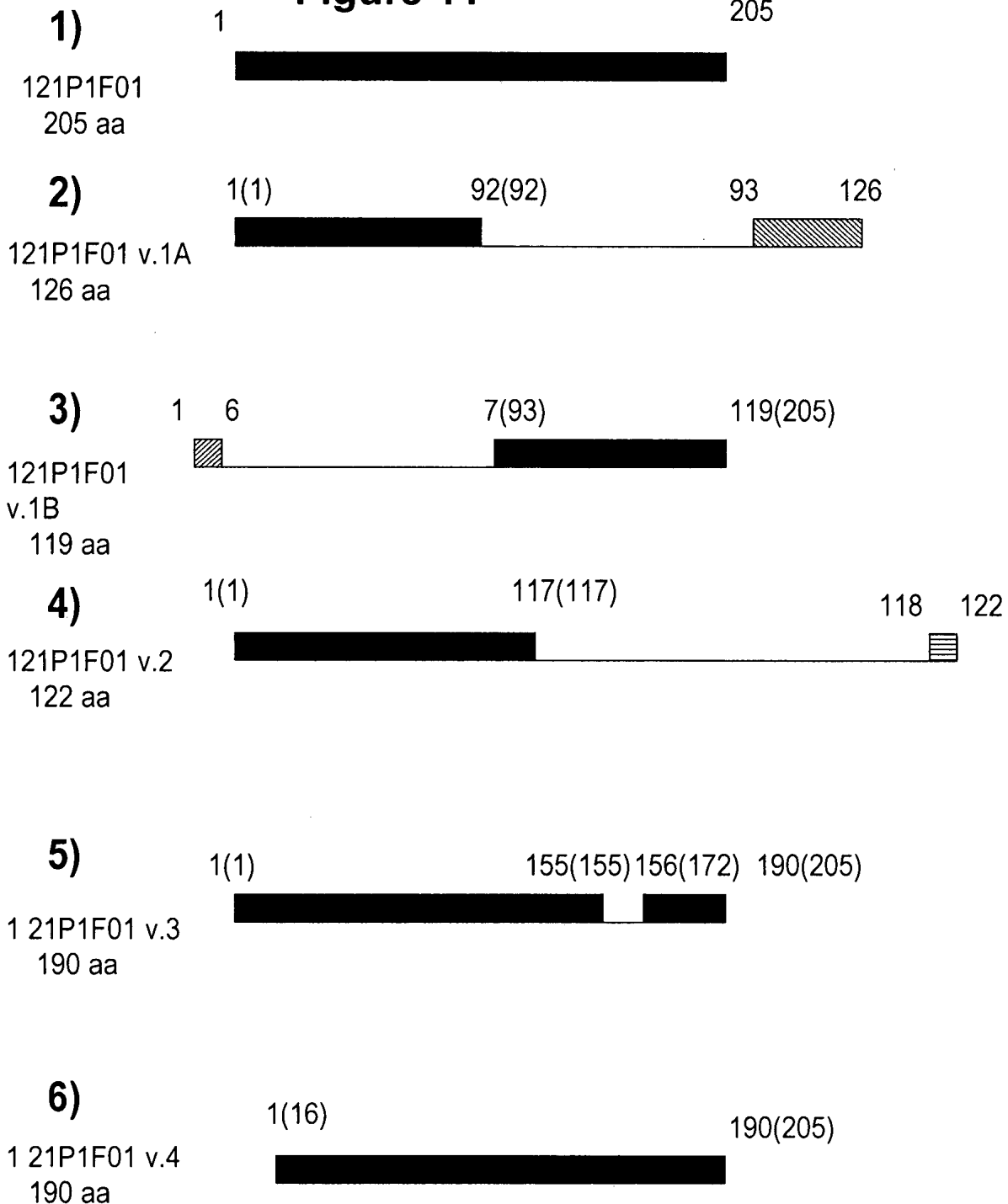


Figure 10



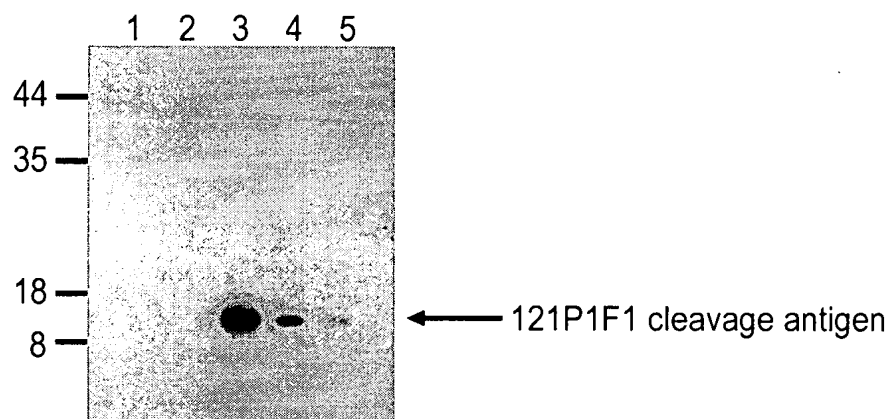
Note: Numbers in “()” correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box.

Figure 11



Note: Numbers in “()” correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

Figure 12
Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb



1. Pre-immune	1:100
2. Pre-immune	1:1,600
3. Anti-121P1F1 serum	1:100
4. Anti-121P1F1 serum	1:400
5. Anti-121P1F1 serum	1:1,600

Figure 13
 Expression of 121P1F1 in various cancer cells

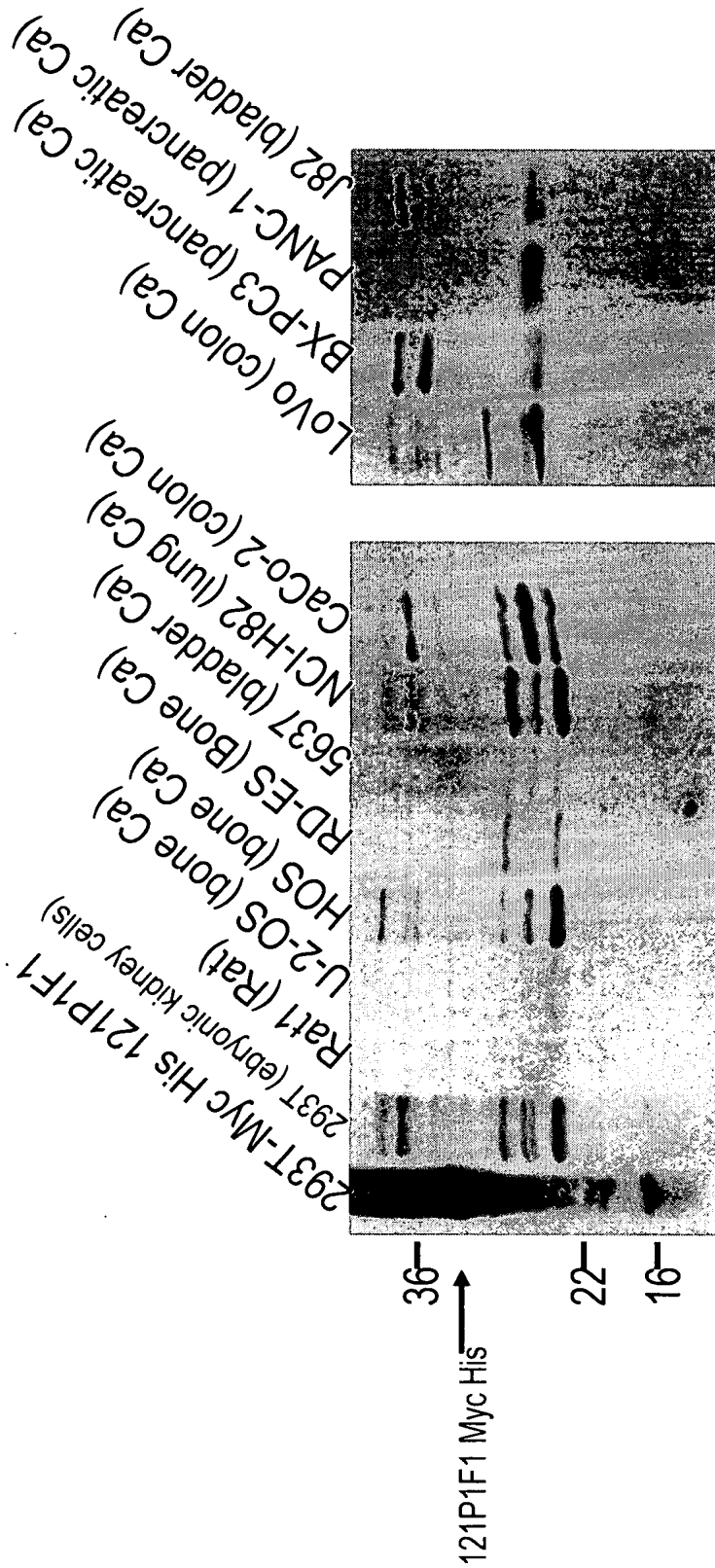


Figure 14 Expression of epitope tagged 121P1F1 in 293T cells

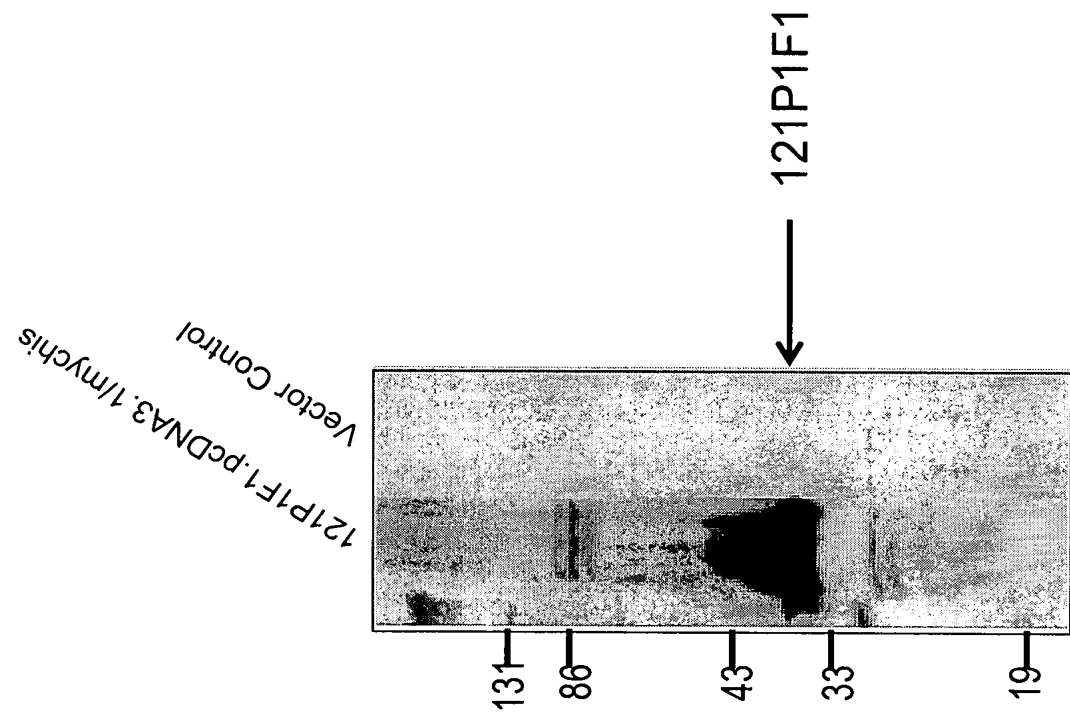


Figure 15 121P1F1 Androgen Regulation *In Vivo*

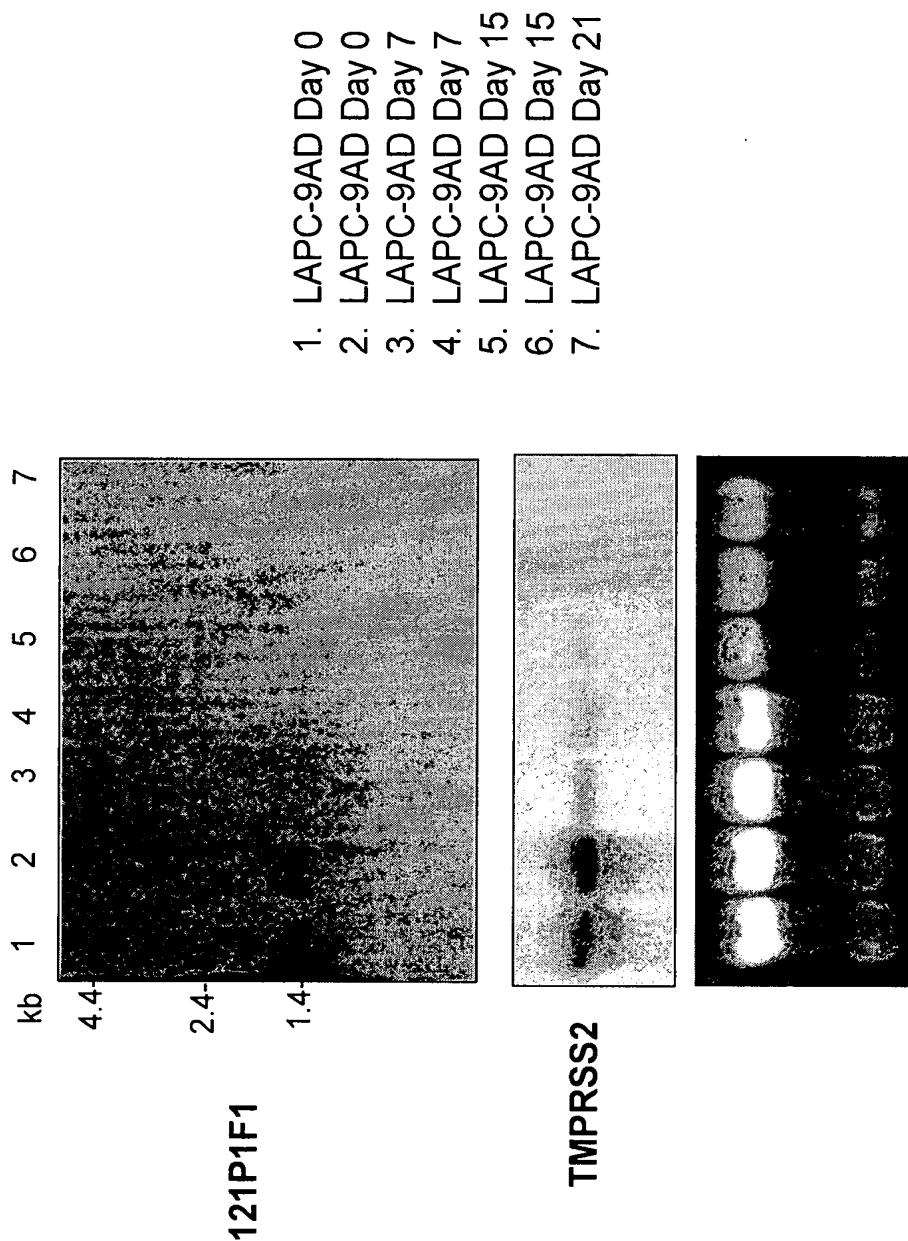


Figure 16A

Secondary structure prediction of 121P1F1

10	20	30	40	50	60	70
MSKKKGLSAEEKTRMMEIFSETKDVQQLKDLEKIAPEKEGITAMSVKEVLQSLVDDGMVDCERIGTSNY						
cc						
YWAFPSKALHARKHKLVELESQSGQKHASLQKSIEKAKIGRCETEERTRLAKESSLRDQREQLKAE						
eecc						
VEKYKDCDPQVVEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGEENKIDRTFGIPEDFDYID						
hhhhcc						

Alpha helix (h) : 61.95% Extended strand (e) : 1.95% Random coil (c) : 36.10%

Figure 16B
 Secondary structure prediction of variant 1a

10	20	30	40	50	60	70
MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLKLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNY						
cc						
YWAFPSKALHARKHKLELVLESQDPGCCFHEIIKVSYYRKFWLGAVAHACNPSTLGG						
eeeecc						

Alpha helix (h) : 50.79% Extended strand (e) : 7.94% Random coil (c) : 41.27%

Figure 17 Expression of 121P1F1 by RT-PCR

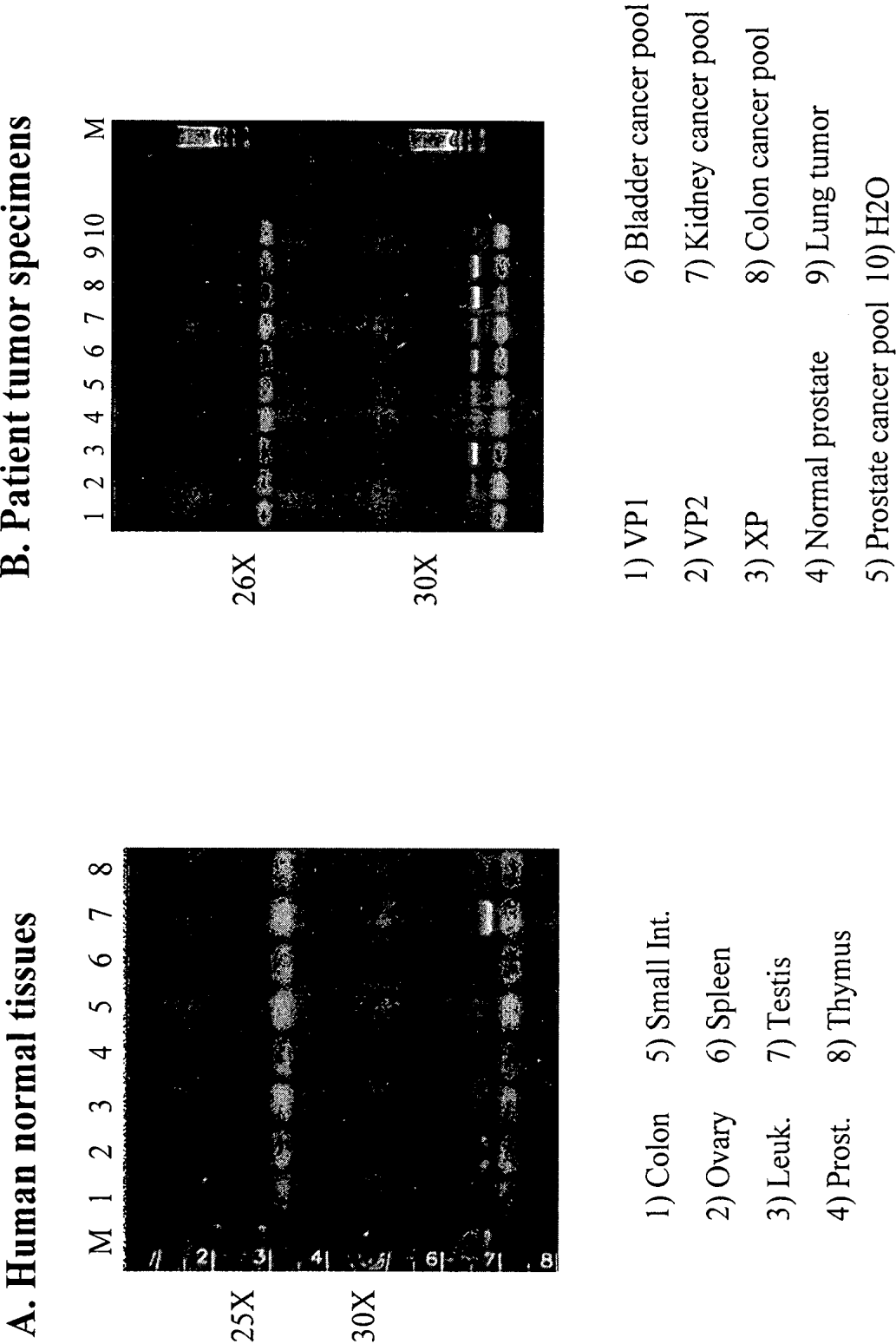


Figure 18 Expression of 121P1F1 in normal human tissues

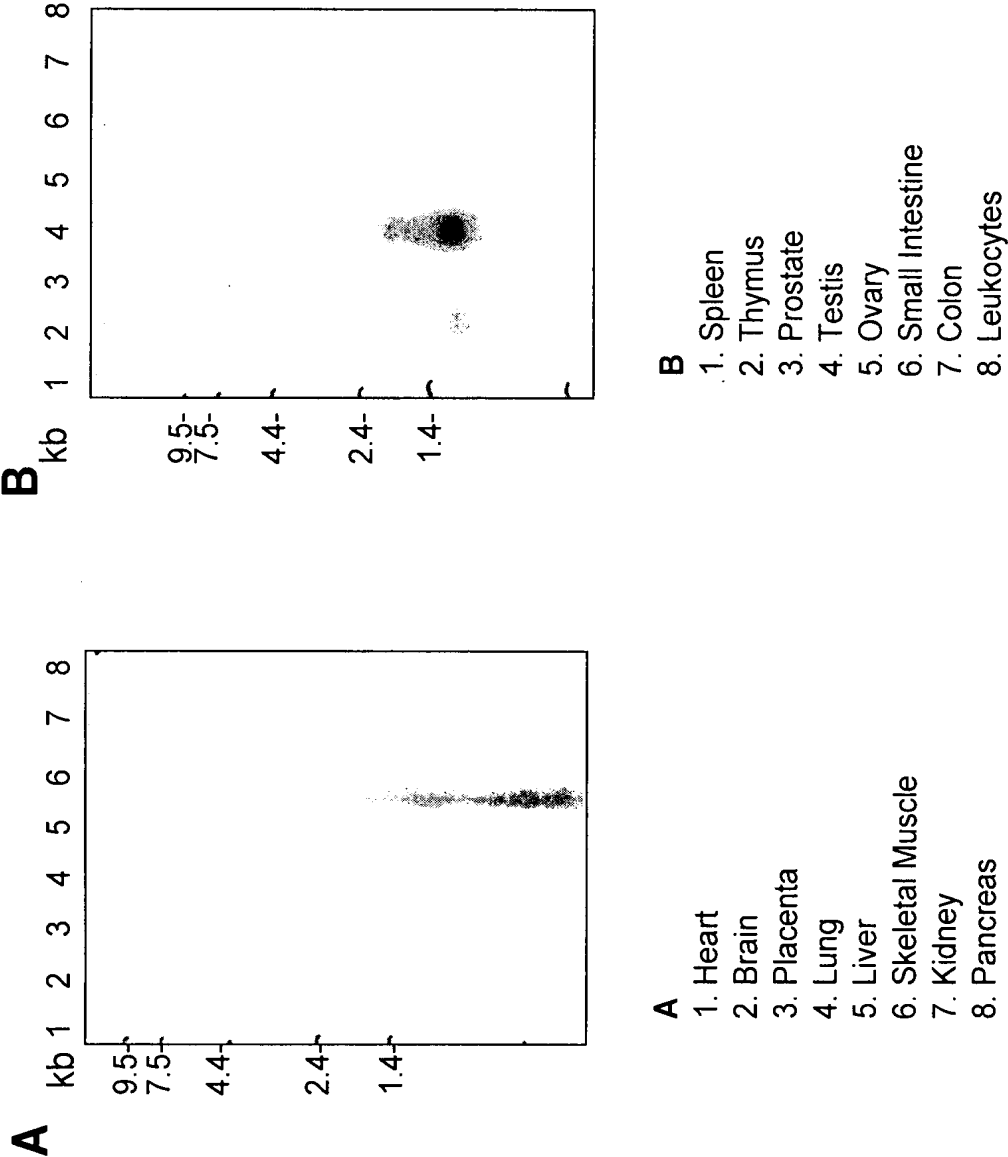


Figure 19 Expression of 121P1F1 in Multiple Cancer Cell lines

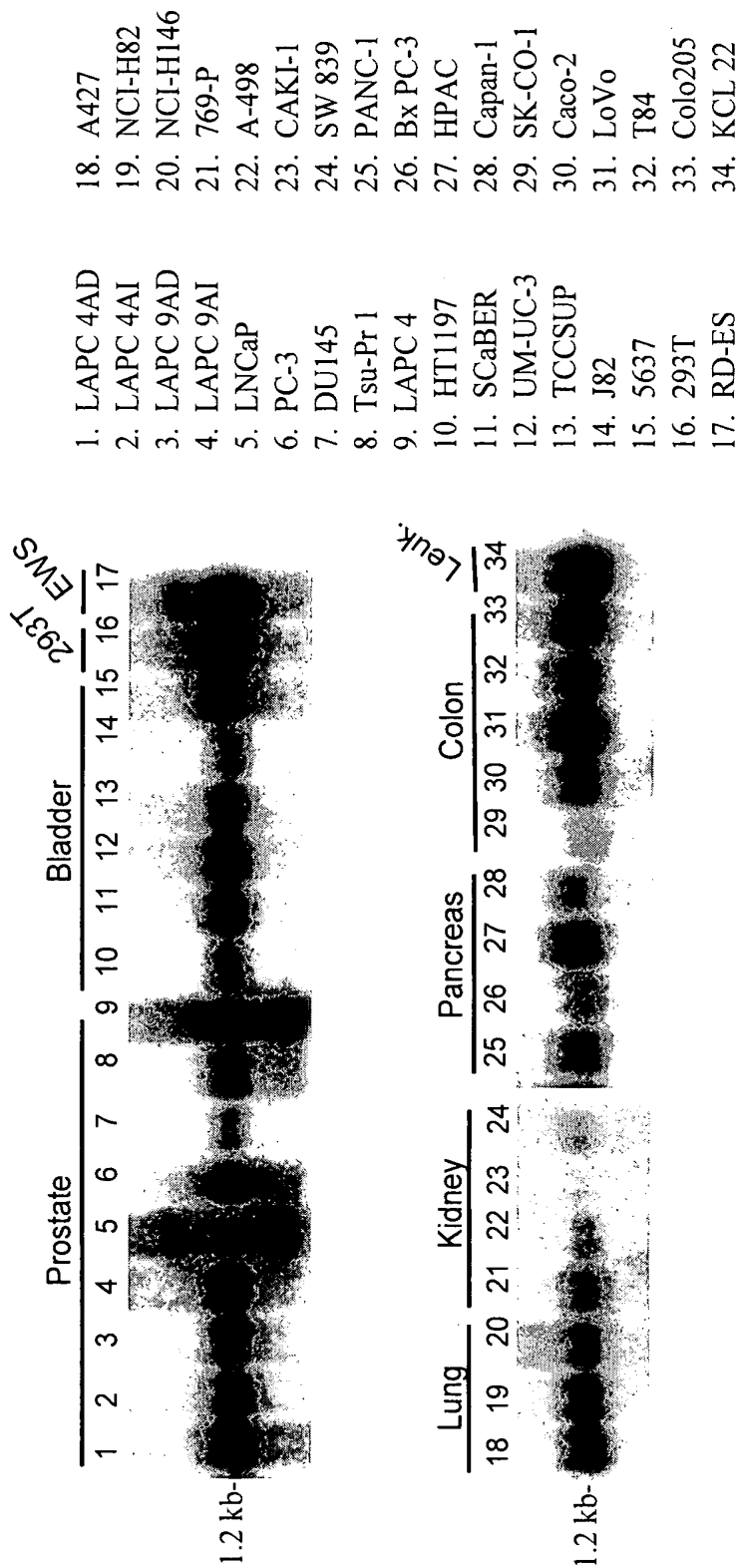


Figure 20 Expression of 121P1F1 in Patient Prostate Cancer Samples

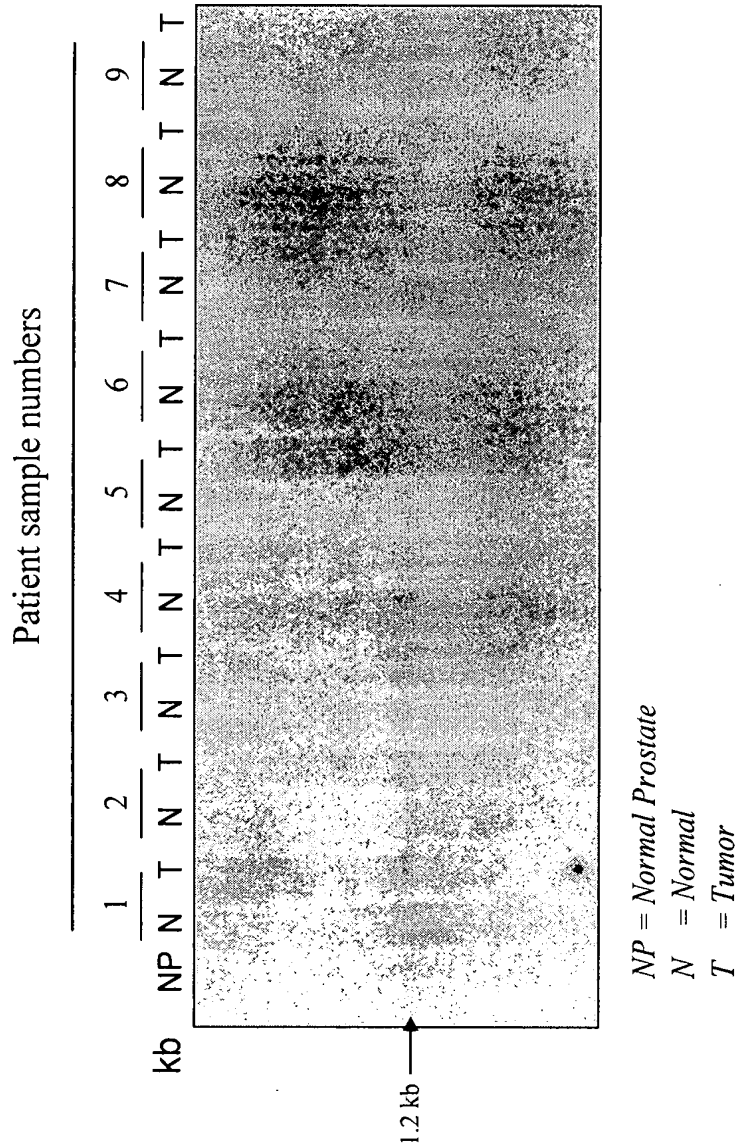


Figure 21 Expression of 121P1F1 in Kidney, Breast, Cervical and Stomach Patients Samples as well as Cancer Cell lines



T = tumor RNA
N = normal adjacent tissue RNA

Cancer cell lines are:
(from left to right)

HeLa (cervical carcinoma)
Daudi (Burkitt's lymphoma)
K562 (CML)
HL-60 (PML)
G361 (melanoma)
A549 (lung carcinoma)
MOLT-4 (lymphoblastic leuk.)
SW480 (colorectal carcinoma)
Raji (Burkitt's lymphoma)

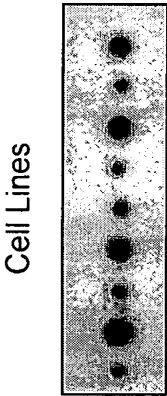


Figure 22 Androgen Regulation of 121P1F1

